amino acid sequence alignments. A consensus sequence, SEQ ID NO:2, was derived from the following overlapping and/or extended nucleic acid sequences: Incyte Clones 989953 (COLNNOT11), 609011, 1226183, and 1227155 (COLNNOT01), 1334268 (COLNNOT13), 1284686 (COLNNOT16), 1391936 (THYRNOT03), (COLNNOT01), 959734 (BRSTTUT03), 892480 (STOMTUT01), and 814959 (OVARTUT01).

Please replace the paragraph beginning at page 12, line 21 and ending on page 13, line 6, with the following rewritten paragraph:

In one embodiment, the invention encompasses the novel human selenium-binding protein, a polypeptide comprising the amino acid sequence of SEQ ID NO:1, as shown in Fig. 1A,B,C. HSEBP is 472 amino acids in length and has no predicted transmembrane domains, potential glycosylation or phosphorylation sites. HSEBP is enriched in leucine and glycine residues which together constitute more than 20% of the total amino acid content. As shown in Fig. 1A,B,C, there are no in-frame TGA termination codons in the nucleic acid sequence of SEQ ID NO:2 to direct the incorporation of selenocysteine into the protein of SEQ ID NO:1. HSEBP has chemical and structural homology with the human fetal heart selenium-binding protein (G1374792; SEQ ID NO:3), mouse liver selenium-binding protein (G227630; SEQ ID NO:4), and mouse liver acetaminophen-binding protein (G298710; SEQ ID NO:5). In particular, HSEBP shares 96%, 86%, and 88% identity, respectively, with each of these proteins. As illustrated by Figs. 3 and 4, HSEBP and human fetal heart selenium-binding protein have rather similar hydrophobicity plots. Their isoelectric points, 5.91 and 6.13, respectively, are also similar. Northern analysis (Fig. 5) shows the expression of the HSEBP sequence in various libraries. Approximately 50% of these libraries are from cancerous tissues and 38% are from the gastrointestinal tract.